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Integration of genetic data on fisheries management models. The European hake case.

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The European hake is one of the major commercially important species in Western Europe fisheries. Currently its management is divided into different functional units in the Mediterranean (GFCM, General Fisheries Commission for the Mediterranean) and two stocks in the Atlantic: the Southern and the Northern Stock. The basis for the definition of this management stock structure is under permanent discussion and in the latest years there were an increased amount of genetic studies addressing this topic. Integrated ecosystem assessment requires an improved understanding of the marine ecosystem to provide an effective advice. To this end we have gathered hake genetic information from different studies with the aim of developing a spatial assessment model that links the current stocks. These studies show a restricted gene flow between Southern hake and Mediterranean hake, although a smaller genetic distance between Southern and Northern stocks than one expected from two independent populations, suggesting the presence of a major gene flow from northern grounds core stock (Porcupine and Great Sole Banks) towards the Bay of Biscay and the northwest coast of the Iberian Peninsula. However the quantitative implementation of genetic metrics (such as F_{st} migration rates, etc) into population dynamic models is not straightforward given the different nature and assumptions behind these different approaches. In this work we discuss the problems to link these different disciplines suggesting ways to overcome them. These include ways to improve future genetic sampling and developing plausible scenarios for genetic connectivity in population dynamic models.

Keywords: European hake, stock, management, genetics

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